



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10796892  
Source: TFWD  
Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS.

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (**EFFECTIVE 12/01/03**):  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

## Raw Sequence Listing Error Summary

**ERROR DETECTED**
**SUGGESTED CORRECTION**
**SERIAL NUMBER:**

10796,892

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is **misaligned**. Do not use tab codes between numbers; use space characters, instead.
- 4  Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for **each** skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
**This sequence is intentionally skipped**  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
**Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.**  
In <220> to <223> section, please explain location of **n or Xaa**, and which residue **n or Xaa** represents.
- 10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11  Use of <220>      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWO

**RAW SEQUENCE LISTING**  
PATENT APPLICATION: US/10/796,892

DATE: 03/22/2004  
TIME: 11:47:18

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\03222004\J796892.raw

3 <110> APPLICANT: Han-Chung Wu  
4 Chin-Tarng Lin  
5 Tong-Young Lee  
W--> 6 <120> TITLE OF INVENTION: A Peptide Marker Targeting To Nasopharyngeal Carcinoma Cell And  
W--> 7 Application Thereof  
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/796,892  
C--> 8 <141> CURRENT FILING DATE: 2004-03-09  
W--> 0 <130> FILE REFERENCE: ~~please insert~~  
W--> 8 <160> NUMBER OF SEQ ID: 2

## ERRORED SEQUENCES

E--> 10 <210> SEQ ID NO **SEQ ID NO: 1** *delete, do not insert alpha, numeric headings.*  
11 <211> LENGTH: 12  
12 <212> TYPE: PRT  
13 <213> ORGANISM: Artificial Sequence  
15 <220> FEATURE:  
16 <223> OTHER INFORMATION: The Peptide Marker Targeting To Nasopharyngeal Carcinoma Cell  
E--> 18 <400> SEQUENCE: 1  
19 Arg Leu Leu Asp Thr Asn Arg Pro Leu Leu Pro Tyr  
E--> 20 1 5 10 *delete, same error*  
E--> 22 <210> SEQ ID NO: **SEQ ID NO: 2** *delete, same error*  
23 <211> LENGTH: 3  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Artificial Sequence  
27 <220> FEATURE:  
28 <223> OTHER INFORMATION: The Peptide Marker Targeting To Nasopharyngeal Carcinoma Cell  
E--> 30 <400> SEQUENCE: 2  
31 Leu Pro Tyr  
32 1

Does Not Comply  
Organism/Sequence Needed  
(PS. 1, 3)

*please see item # "3" on error  
Summary sheet.*

**RAW SEQUENCE LISTING ERROR SUMMARY**  
PATENT APPLICATION: US/10/796,892

DATE: 03/22/2004  
TIME: 11:47:19

Input Set : A:\PTO.KD.txt  
Output Set: N:\CRF4\03222004\J796892.raw

**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:0; Line(s) 6

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/796,892

DATE: 03/22/2004

TIME: 11:47:19

Input Set : A:\PTO.KD.txt

Output Set: N:\CRF4\03222004\J796892.raw

L:6 M:283 W: Missing Blank Line separator, <120> field identifier  
L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE  
L:8 M:283 W: Missing Blank Line separator, <160> field identifier  
L:10 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:18 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1 ✓  
L:20 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1✓  
L:22 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO ✓  
L:30 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:2 ✓